



SEQUENCE LISTING

<10> Carrino, John J.
Gerrue, Louis O.
Diver, Jonathan M.

<120> Multiplex Amplification and Separation of Nucleic Acid
Sequences Using Ligation-Dependant Strand Displacement
Amplification and Bioelectronic Chip Technology

<130> 265/018 Nanogen

<140> 09/865,807

<141> 2001-05-25

<160> 62

<170> PatentIn version 3.1

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<212> DNA

<213> Conserved 16S bacterial sequence

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<211> 15

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<213> Homo sapiens

09865807 000701

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Figure 1. The 12 test cases of the proposed algorithm. The first column shows the input images, the second column shows the detected edges, and the third column shows the detected corners. The images are labeled as follows: (a) 1, (b) 2, (c) 3, (d) 4, (e) 5, (f) 6, (g) 7, (h) 8, (i) 9, (j) 10, (k) 11, (l) 12.

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[illegible]

[illegible]

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<211> 42

<213> Chlamydia trachomatis

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17

<211> 19

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<211> 16

<213> Chlamydia trachomatis

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16

<211> 42

<213> Homo sapiens

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42

Figure 1. The structure of the *hsp70* gene. The exons are numbered 1 to 5. The introns are numbered 1 to 4. The size of the exons and introns is indicated in base pairs (bp). The size of the gene is indicated in base pairs (bp). The size of the gene is indicated in base pairs (bp).

42

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45

<213> Salmonella

<400> 38

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tcgccttagc 70

<210> 39

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<212> DNA

<213> Artificial sequence

<220>

<223> Amplification primer

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<210> 40

<211> 40

<212> DNA

<213> Artificial sequence

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<400> 41

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<210> 42

<211> 42

<212> DNA

<213> Homo sapiens

<400> 42

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<210> 43

<211> 42

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<213> Homo sapiens

<400> 43

acgattcagc tccagacttc tccggtcaga atttctgaaa gg 42

<210> 44

<211> 21

102030-2035560

Figure	Figure	Figure	Figure	Figure	Figure	Figure	Figure	Figure	Figure
Figure 1	Figure 2	Figure 3	Figure 4	Figure 5	Figure 6	Figure 7	Figure 8	Figure 9	Figure 10

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<210> 62
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